

OIPE

			DATE: 01/19/2002
		PATENT APPLICATION: US/10/037,598	TIME: 11:52:15
		Input Set : A:\ES.txt Output Set: N:\CRF3\01182002\J037598.ra w	ρ,5
3	<110>	APPLICANT: Monsanto Co	\
4		Concibido, Vergel	
5		Delanney, Xavier	
7	<120>	TITLE OF INVENTION: Soybean Plants with Enhance	d Yields and Methods for Breeding
for and			
8		Screening of Soybean Plants with Enhanced Yield	s
		FILE REFERENCE: 38-21(52175)B	
C> 12	<140>	CURRENT APPLICATION NUMBER: US/10/037,598	_
C> 12	<141>	CURRENT FILING DATE: 2002-01-04	Does Not Comply
12	<150>	PRIOR APPLICATION NUMBER: (05/260,040	Corrected Diskette Needed
		PRIOR FILING DATE: 2001-01-05	100000
		NUMBER OF SEQ ID NOS: 37	
		SOFTWARE: PatentIn version 3.0 SEQ ID NO: 1	
		LENGTH: 24	
		TYPE: DNA	
		ORGANISM: Glycine max	
		SEQUENCE: 1	
		acaac tctaatgaaa atct	24
		SEQ ID NO: 2	24
		LENGTH: 23	
		TYPE: DNA	
31	<213>	ORGANISM: Glycine max	
		SEQUENCE: 2	
34	gcggag	gtttg atttttcaaa agt	23
37	<210>	SEQ ID NO: 3	
38	<211>	LENGTH: 25	
		TYPE: DNA	
		ORGANISM: Glycine max	
		SEQUENCE: 3	
		taat ttatgatata accaa	25
		SEQ ID NO: 4	
		LENGTH: 24	
		TYPE: DNA	
		ORGANISM: Glycine max SEQUENCE: 4	
52	acattt	tate tetttteea caac	24
55	<210>	SEQ ID NO: 5	24
		LENGTH: 25	
		TYPE: DNA	
		ORGANISM: Glycine max	
		SEQUENCE: 5	
		cgac gcaataatca agaaa	25
		SEQ ID NO: 6	

Input Set : A:\ES.txt

Output Set: N:\CRF3\01182002\J037598.raw

65 <211> LENGTH: 25	
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74 <211> LENGTH: 25	
75 <212> TYPE: DNA	
76 <213> ORGANISM: Glycine max	
78 <400> SEQUENCE: 7 79 caggetteag tgtgeataat acagg	0.5
82 <210> SEQ ID NO: 8	25
83 <211> LENGTH: 25	
84 <212> TYPE: DNA	
85 <213> ORGANISM: Glycine max	
87 <400> SEQUENCE: 8	
88 ttctatgttc cctgtgcaaa cactg	25
91 <210> SEQ ID NO: 9	
92 <211> LENGTH: 25	
93 <212> TYPE: DNA	
94 <213> ORGANISM: Glycine max	
96 <400> SEQUENCE: 9	
97 gtctgcaagc taacagtgtc agagg	25
100 <210> SEQ ID NO: 10	
101 <211> LENGTH: 26	
102 <212> TYPE: DNA	
103 <213> ORGANISM: Glycine max	
105 <400> SEQUENCE: 10	
106 cacactcaat ctcattagca gacacg	26
109 <210> SEQ ID NO: 11	
110 <211> LENGTH: 25 111 <212> TYPE: DNA	
111 \Z12> TIPE: DNA 112 \<213> ORGANISM: Glycine max	
114 <400> SEQUENCE: 11	
115 teetttgget cactattgac gattt	25
118 <210> SEQ ID NO: 12	25
119 <211> LENGTH: 25	
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121 <213> ORGANISM: Glycine max	
123 <400> SEQUENCE: 12	
124 acceptgtge cactttaact acatt	25
127 <210> SEQ ID NO: 13	
128 <211> LENGTH: 25	
129 <212> TYPE: DNA	
130 <213> ORGANISM: Glycine max	
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136 <210> SEQ ID NO: 14	
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	<210> SEQ ID NO: 15	
	<211> LENGTH: 28	
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	<400> SEQUENCE: 15	
	gcggacaatt ttttatcaat aatttatt	28
	<210> SEQ ID NO: 16	
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	<212> TYPE: DNA	
	<213> ORGANISM: Glycine max <400> SEQUENCE: 16	
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	gcgatgctta cttttcctat gatcactt <210> SEQ ID NO: 17	28
	<211> LENGTH: 24	
	<211> DENGIII. 24 <212> TYPE: DNA	
	<213> ORGANISM: Glycine max	
	<400> SEQUENCE: 17	
	gcgtagcaac aaagcaatct acag	24
	<210> SEQ ID NO: 18	24
	<211> LENGTH: 29	
	<212> TYPE: DNA	
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	<400> SEQUENCE: 18	
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	<210> SEQ ID NO: 19	
182	<211> LENGTH: 235	
183	<212> TYPE: DNA	
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189	acgaagttcc cttaaaaaat ctttagtaag ac	acatgcat taattatatg acaataaaaa 120
191	aaaaaagaat tcaaatgttt caaaatgaaa aa	tcattaat tcacttttat gtcaattatt 180
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	<210> SEQ ID NO: 20	
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	<213> ORGANISM: Glycine max	
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204		
206	attattatta ttattattat tattattaaa ag	ttatacat gtaaatattt ttttaaggtg 120
200	acattctgaa taaattttta tatgtgattt gg	gaaaagta gagacaagtt caccctaaaa 180
208	acattotgaa taaattttta tatgtgattt gg ttaatattoa gtaagtggaa cgtotocaaa tt	gaaaagta gagacaagtt caccctaaaa 180 tattataa aaattgtaaa tatttattct 240
208 210	acattotgaa taaattttta tatgtgattt gg ttaatattoa gtaagtggaa ogtotocaaa tt atgogactga agttgtggaa aaagagataa aa	gaaaagta gagacaagtt caccctaaaa 180
208 210 213	acattotgaa taaattttta tatgtgattt gg ttaatattoa gtaagtggaa cgtotocaaa tt	gaaaagta gagacaagtt caccctaaaa 180 tattataa aaattgtaaa tatttattct 240

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215	<212> TYPE: DNA								
216	<213> ORGANISM: Glycine max								
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219	atcaatcgac gcaataatca agaaaatcaa a	acatggtatc agtaattaat tttaaataag	60						
	attatatata tatatatata tatatatata t		120						
	taaaaatcat attaaaacaa ttataattca t		180						
	taaatggcaa cacctcatcg tattcaaata a		240						
	ttttggttcc tggaatgaca tcccattgtc t		280						
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	<211> LENGTH: 366								
	<212> TYPE: DNA								
	<213> ORGANISM: Glycine max								
	<400> SEQUENCE: 22								
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230	caggetteag tgtgcataat acaggtttet g	judgetggga ctttctccca acatttcatt	60						
	ttgggatttt ctcccaacct ttattttgtc t		120						
	ttccttcctt catgtttcat tcgtgatcct g		180						
242	cctagtaggg ggccaggtgt caacctatag t	tgggatttc accepttagg ctgaaatttc 🤭	240						
	ctttcctcac ttaagtaaaa aaaaaaacaa a		300						
	tttatagcaa ttttatatga ttagaaaatt a	aactattcc ccagtgtttg cacagggaac	360						
	atagaa		366						
	<210> SEQ ID NO: 23								
252	<211> LENGTH: 96								
253	<212> TYPE: DNA								
254	<213> ORGANISM: Glycine max								
256	<400> SEQUENCE: 23								
257	gtctgcaagc taacagtgtc agaggatatg a	atattagta ttattaacaa taataataat	60						
	aatgatgaaa cgtgtctgct aatgagattg a		96						
262	<210> SEQ ID NO: 24								
263	<211> LENGTH: 321								
264	<212> TYPE: DNA	·							
265	<213> ORGANISM: Glycine max	•							
	<400> SEQUENCE: 24	•							
268	teetttgget cactattgae gatttteteg a	tgattaatt gacccaacat tctgtttgta	60						
270	actttatta taaaacaaat atttgtactt c	aattataac aacaaattta agaagaatat	120						
	atatatat atatttgtga tggaaatgat c		180						
	aatcaagaaa aataatagac tcatttattt c	2 3 3	240						
	tacaaatggt aaacataaaa gaaaaaaaaa c		300						
	tagttaaagt ggcacacggg t		321						
	<210> SEQ ID NO: 25		321						
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	<400> SEQUENCE: 25								
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	taacgetgea tgatttgagt tetgttttgt co		60						
	gttagttaat ttgtatattt attggtgata to		120						
	gtgtgtgtgt gtggtagtga gaagaattga ga		180						
	aatac	•	185						
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29/	<211> LENGTH: 3830								

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299 <213> ORGANISM: Glycine max
301 <400> SEQUENCE: 26
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304 aatgtcaagt gagtttagaa tactaaatga aaattttaac ataaaaaaaa aaaaatcaat
                                                                      180
306 ggaatggaac ccatccagcg caactagctg agtcacatac agtgccaaaa gacatgggta
308 ctacaaatgc tcactttagt ggctatggaa caaccatcag cattcagctc ttcctttttt
                                                                      240
                                                                      300
310 ctgtcgtagg ccaagagaca aagtttgtca caggtttaca aattgattgt ggccacaatc
312 acacggtaaa cattagaatg gaagaaaaaa aatctgtcta tgatcgatgt cgtgaacttc
                                                                      360
314 acccactcca tcaatgaaga atttatttta aatacagtta cacaccaact taataagact
                                                                      420
316 ttttgcacaa aattacctga ttgggaggaa tatgaattgt cttataaatc acgtattcac
                                                                      480
318 aagttetact tttacaaaac tetttacatg tattttecaa aaaaagaaaa atetttacat
                                                                      540
320 gtatgttaac ctacctaaca aatctctaat taacctataa attttttaaa tgctttttga
                                                                      600
                                                                      660
322 qaaaacttta taqqcaqata qaaqattgtt gagagttttt taaatgctta tcaacaatct
324 ccgatagtcc cttagcttta ccaagtacat gaaaatctta catataatgc ttttacttta
                                                                      720
326 ccaactatta acttgagcac cgaaatcttt accagtatgc tcatttgatg catattaaaa
                                                                      780
328 tgtacaaaat tttatagagg cctgatcaat accatcgaat gaaaccttaa tgacatgcta
                                                                      840
330 cttqttagcg atgtcaataa aggcttactc aaggattatt ccacaggcct aaatcataga
                                                                      900
332 caattttact taattqtatt tattcaatta qtccttagat qtcaaagaat ctattagatg
                                                                      960
                                                                     1020
334 atagttttag tggcatgata gagaatgaaa cccacatcta taaaaaaaaag aagacaaaag
336 ttagttttag atctttaatc acttgtgtga attcatatta gttttacgtg tattcgaagt
                                                                     1080
                                                                     1140
338 gaaaatattc atctgtatga gaccataaac attcttatga gagacttgtt tgaagtataa
                                                                     1200
340 tttttcatag tacagtaaag ctgattgttg ttttttctcg tacgcaaaat ttatattcag
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342 gacaatgttt aagagtgaaa acataataaa attaacctca caaaaagtaa gtatatatat
1320
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346 ataaatagat totoacaaaa tataatttat tattaaatta atttttaaca ttataactta
348 acgataaaat attttttta tatttttta tgaactaatt taacaactca tcacatcttg
                                                                     1440
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352 atttagcatc tttttgggag aatactaaaa aacatataaa agaaaaagaa atattcagga
                                                                     1560
354 tgaaaaatga aatgcgtgtg aaaattggaa ggaggtaagg ctgggtcgac ccagatctag
                                                                     1620
356 ttgagctcac caactcccgc tcccatttcc ttatttatag acagagtctg attgtttcct
                                                                     1680
                                                                     1740
358 caccactece tecactetet ttetetagte etgttattte teagegegta aageatgget
360 ttgttggtgg agaaaaccac gagtggtcgc gagtacaagg tcaaggacct ttcccaggcc
                                                                     1800
362 gacttcggcc gcctcgagat cgagctggcc gaggttgaga tgcccggcct catggcctgt
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364 cggaccgagt tcggcccctc ccagcccttc aagggggccc gcatcaccgg ctccctccac
                                                                     1920
                                                                     1980
366 atgaccatec agaccqccqt teteattgag acceteaceg ccettggcge egaggteege
                                                                     2040
368 tgqtqctcct qcaacatctt ctccacccag gaccacgccg ccgccgctat tgcccgcgac
                                                                     2100
370 agtqccqccq tcttcqcctq gaagggtgag accctccagg agtactggtg gtgcaccgag
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372 egegeeteg actggggeee eggtggtgga eeegaeetea tegtegaega eggtggtgae
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374 gctaccette teatecaega aggegteaag geegaggage tetatgagaa gaeeggegaa
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376 ctccccgacc ccaactccac cgacaacgcc gagtttcaga tcgtgcttac catcateaga
                                                                     2340
378 gatgggttga agaccgatcc caccaggtac cgcaagatga aggagcgtct cgttggggtt
380 tetgaggaaa ceaceaetgg agttaagagg etetateaga tgeaggegaa tgggaetett
                                                                     2400
                                                                     2460
382 ctcttccctg ctattaatgt caatgactct gtcaccaaga gcaaggtaat gtctcttttt
384 cccccagatc tagtgtcttt tttgtgttaa aatgtaggat tgagttcgga tctgttgttt
                                                                     2520
386 ttggatgggt tttgtgccat tggtgaaatg aggttttgaa cctgtcaact gtttgactaa
                                                                     2580
388 tgtcctctaa gaagtctgga tcggtattgg gtgctatttt agtgtgtttg gatctgtgtg
                                                                     2640
390 ttgaaacgtc agaacattag taagttgctt gctaacgtga ctttaggtaa atggtcacat
                                                                     2700
2760
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Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARYDATE: 01/19/2002PATENT APPLICATION: US/10/037,598TIME: 11:52:16

Input Set : A:\ES.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34